<u>**Amendments to the Claims**</u>

This listing of claims will replace all prior versions and listings of claims in the application.

<u>**Listing of Claims:**</u>

Claim 1 (Currently amended):   A method for modeling cellular metabolism of an organism, comprising:

constructing a flux balance analysis model utilizing stoichiometric mass balances of metabolic

and cellular composition information to identify boundaries for available flux

distributions <u>of a metabolic network; and</u>

applying logic constraints to the flux balance analysis model ~~to thereby tighten the boundaries~~

~~for the available flux distributions~~ <u>to produce an altered flux balance analysis model, wherein</u>

<u>said logic constraints constrain a boundary for an available flux distribution to thereby</u>

<u>improve predictive capabilities of said flux balance analysis model</u>.

Claim 2 (Previously presented):   The method of claim 1 wherein at least a subset of the logic constraints are capable of protecting against violation of a kinetic barrier.

Claim 3 (Previously presented):   The method of claim 1 wherein the logic constraints further include a set of connectivity restraints.

Claim 4 (Currently amended):   The method of claim 1 further comprising the step of applying mixed-integer linear programming to <u>said flux balance analysis model having improved predictive capabilities to</u> solve for a desired metabolic outcome.

Claim 5 (Original):   The method of claim 1 further comprising the step of solving for a desired metabolic outcome.

Claim 6 (Currently amended):   A method for modeling cellular metabolism of an organism that improves upon a flux balance analysis model, comprising:

constructing the flux balance analysis model utilizing stoichiometric mass balances of metabolic and cellular composition information to identify boundaries for available flux distributions of a metabolic network; and

applying a plurality of logic constraints to the flux balance analysis model to ~~thereby tighten the boundaries for the available flux distributions~~ produce an altered flux balance analysis model, wherein said plurality of logic constraints constrain a boundary for available flux distributions to thereby improve predictive capabilities of said flux balance analysis model.

Claim 7 (Currently amended):   The method of claim 6, further comprising selecting the set of logic constraints to protect against violation of a kinetic or regulatory barrier.

Claim 8 (Original):   The method of claim 6 wherein the logic constraints are defined by a relationship between changes in reaction fluxes and metabolic concentrations.

Claim 9 (Cancelled).

Claim 10 (Original):   The method of claim 6 wherein the logic constraints are represented by binary variables.

Claim 11 (Original):   The method of claim 10 wherein a first binary variable represents the presence of a reaction and a second binary variable represents the absence of a reaction.

Claim 12 (Original):   The method of claim 6 further comprising applying a computational procedure to identify a minimal set of metabolic reactions.

Claim 13 (Original):   The method of claim 12 further comprising selecting a growth rate, and wherein the step of applying a computational procedure is applying a computational procedure to identify the minimal set of metabolic reactions capable of supporting the growth rate.

Claim 14 (Currently amended):   The method of claim 6 further comprising the step of applying mixed-integer linear programming to said flux balance analysis model having improved predictive capabilities to solve for a desired metabolic outcome.

Claim 15 (Previously presented):   The method of claim 6 further comprising the step of solving for a desired metabolic outcome.

Claim 16 (Currently amended):   The method of claim 15 further comprising engineering the a change in an organism based on the desired metabolic outcome.

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Claims 17-18 (Cancelled).

Claim 19 (Currently amended):   A system for modeling cellular metabolism of an organism, comprising:

a flux balance analysis model contained on a computer readable medium utilizing stoichiometric

      mass balances of the metabolic and cellular composition information to identify

      boundaries for available flux distributions of a metabolic network;

a plurality of logic constraints applied to the flux balance analysis model to tighten the

      boundaries for available flux distributions, the logic constraints selected from the set

      consisting of qualitative kinetic information constraints, qualitative regulatory

      information constraints, and differential DNA microarray experimental data constraints;

      and

commands for producing an altered flux balance analysis model wherein said plurality of logic

      constraints constrain a boundary for available flux distributions to thereby improve

      predictive capabilities of said flux balance analysis model.

Claim 20 (Previously presented):   The method of claim 1 wherein the logic constraints further include qualitative regulatory information constraints.

Claim 21 (Currently amended):   The method system of claim 20 wherein at least a subset of the logic constraints protect against violation of a regulatory barrier.

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Claim 22 (Currently amended): The ~~system~~ method of claim 1 wherein the logic constraints further include DNA experimental data constraints.

Claim 23 (Currently amended): A method for modeling cellular metabolism of an organism, comprising:

constructing a flux balance analysis model of a metabolic network;

applying constraints to the flux balance analysis model, wherein the constraints include

qualitative kinetic information constraints, qualitative regulatory information constraints,

~~and~~ differential DNA microarray experimental data constraints, or a combination thereof;

and

producing an altered flux balance analysis model wherein said constraints constrain a boundary

for an available flux distribution to thereby improve predictive capabilities of said flux

balance analysis model.

Claim 24 (Previously presented): The method of claim 23 wherein the constraints include logic constraints to protect against violation of a regulatory barrier.

Claim 25 (Previously presented): The method of claim 23 wherein the constraints further include connectivity restraints.

Claim 26 (Currently amended): The method of claim 23 further comprising applying mixed-integer linear programming to said flux balance analysis model having improved predictive capabilities to solve for a desired metabolic outcome.

Claim 27 (Previously presented):   The method of claim 23 further comprising solving for a desired metabolic outcome.

Claims 28-29 (Cancelled).

Claim 30 (Currently amended):   A method for modeling cellular metabolism of an organism that improves upon a flux balance analysis model, comprising:

constructing the flux balance analysis model utilizing stoichiometric mass balances of metabolic

     and cellular composition information to identify boundaries for available flux

     distributions of a metabolic network;

applying a plurality of logic constraints to the flux balance analysis model to ~~tighten the~~

     ~~boundaries~~ produce an altered flux balance analysis model, wherein said plurality of logic

     constraints constrain a boundary for available flux distributions to thereby improve

     predictive capabilities of said flux balance analysis model; and

applying mixed-integer linear programming to said flux balance analysis model having improved

     predictive capabilities to solve for a desired metabolic outcome ~~associated with~~ of the

     flux balance analysis model of the organism.

Claim 31 (Previously presented):   The method of claim 30 further comprising the step of solving for the desired metabolic outcome.

Claim 32 (Previously presented):   The method of claim 31 further comprising engineering a

change in the organism based on the desired metabolic outcome.

Claim 33 (Currently amended):   A method for modeling cellular metabolism of an

organism, comprising:

constructing a flux balance analysis model using stoichiometric mass balances of metabolic and

    cellular composition information to identify stoichiometric boundaries for available flux

    distributions of a metabolic network;

determining logic constrains to apply to the flux balance analysis model to tighten the

    stoichiometric boundaries, the logic constraints based on qualitative relationships

    between changes in reaction fluxes and changes in metabolite concentrations; and

applying the logic constraints to the flux balance analysis model to thereby tighten the

    stoichiometric boundaries produce an altered flux balance analysis model, wherein said

    logic constraints constrain a boundary for an available flux distribution to thereby

    improve predictive capabilities of said flux balance analysis model.

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